

V. Bortner

RAW SEQUENCE LISTING DATE: 11/28/2000
PATENT APPLICATION: US/09/252,691C TIME: 12:05:30

Input Set : D:\Pat9903.pto
Output Set: N:\CRF3\11282000\I252691C.raw

PH18

4 <110> APPLICANT: Keith G. Weinstock et al.
6 <120> TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
7 CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
9 <130> FILE REFERENCE: 107196.135
11 <140> CURRENT APPLICATION NUMBER: US 09/252,691C
12 <141> CURRENT FILING DATE: 1999-02-18
14 <150> PRIOR APPLICATION NUMBER: US 60/094,145
15 <151> PRIOR FILING DATE: 1998-07-24
17 <150> PRIOR APPLICATION NUMBER: US 60/074,787
18 <151> PRIOR FILING DATE: 1998-02-18
21 <160> NUMBER OF SEQ ID NOS: 11326
24 <210> SEQ ID NO: 1
25 <211> LENGTH: 432
26 <212> TYPE: DNA
27 <213> ORGANISM: Enterobacter cloacae
29 <400> SEQUENCE: 1
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31 tctggctgtgt gtgcgcgcctg ttgcgcctcg tttttgtttgg gtgttcctcc tggggcggtct 120
32 tgcgtccccctg ctgcgtcccccgg ttgcgcgtttt tcctgtcggt ttgttccttc cgctactgcc 180
33 ggcgttcgtgt ttatatttagt cgtggcgctg ttgttcgtgt tggttcgtgt ctgtttccg 240
34 gttcgttcgt ttgggttcgt gtgcgcgtcc ttgttcctgg tcctgcgttt cctgtggcg 300
35 ctgtggatgg atcagggggtt ggtgtgtgtgg ctgcgtcaag tcgtgtggc gccggaaagc 360
36 cataaaaaacc cggtgacgtt ggtgatcaag gggcttatcc tcgtgtccat tggtggta 420
37 gtgtatgttc tg 432
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 231
41 <212> TYPE: DNA
42 <213> ORGANISM: Enterobacter cloacae
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45 <221> NAME/KEY: unsure /
46 <222> LOCATION: (217)
48 <220> FEATURE:
49 <221> NAME/KEY: unsure /
50 <222> LOCATION: (218)
52 <400> SEQUENCE: 2
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54 caggggacca agacgcgcggcca ggaggagaac ccaacaaaaa cgaaggcgaa caggcgccgac 120
55 agcagccaga acaccagcag agacacaaaag accaccgggg cgacgcgcgtt ccagaaagac 180
56 ggcgacaaca tcagcacgaa gaagacgaaac cgggacmaa atcgtaactta a 231
58 <210> SEQ ID NO: 3
59 <211> LENGTH: 490
60 <212> TYPE: DNA
61 <213> ORGANISM: Enterobacter cloacae
63 <400> SEQUENCE: 3
64 ccccaaaagg aqcgaggccc tcggcgccac aatcgccaga gggatggta atacccagac 60
65 cgggtcaggag gagaagaaag tcggcagcgc cggatcgag cggaaagacgc ccccggtcg 120
66 caccqqqqcq qaaqqaqaqq cqaaaqgcga qaactcgcg cggaaaqgcgg aqaaqgcga 180

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See p. 5

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7 E 13

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67 atccggctca	ccgaaagaaa	gcaggaaaggc	ggagaaaaacg	gaggcagagca	tccggcgaggaa	240
68 ggcggtaaaa	acgcggcgca	agatccageg	gcagcagatc	caggacgggc	agaaaagcggc	300
69 cagtccagggt	aacgcgcgacg	aggcqaaacg	gatccggctc	ggcaaaccgg	aayatttcac	360
70 acqattcat	caggccggca	ggatccggca	gccgcacata	acctccgcac	cctttaacgt	420
71 tcaggcgatg	atgcgtcatcg	ccccctggtct	tcacccgtcg	actggacgg	tacgcgcata	480
72 tgtagttt						490
74 <210>	SEQ ID NO:	4				
75 <211>	LENGTH:	267				
76 <212>	TYPE:	DNA				
77 <213>	ORGANISM:	Enterobacter cloacae				
79 <400>	SEQUENCE:	4				
80 aycagtggtt	ggccggcagga	aaatccgccta	tctgtggcga	acagcattgg	tcaggatcg	60
81 cgttccctgt	ttaagtatc	gcccggatcty	gagtcctact	tccactactcg	ctatctggat	120
82 gtgagcaccc	tgaaaagact	ggcccccgcgc	tggaaaaccgg	aaattttca	cggttccaca	180
83 aaggcagggg	cgcacccggc	gatggatgac	atccgtgagt	ctgttgcgg	gctggcgtac	240
84 tatecgcaaa	acttttattaa	gtctctg				267
86 <210>	SEQ ID NO:	5				
87 <211>	LENGTH:	393				
88 <212>	TYPE:	DNA				
89 <213>	ORGANISM:	Enterobacter cloacae				
91 <400>	SEQUENCE:	5				
92 cctgctactg	ccggtaatgc	gagaagggt	gaaaataaca	ttagcgcgg	cgaaaacaa	60
93 ctgattttgga	tgcgtatgg	gtggaccggc	cttgatcccg	agcgcgtatcg	cattatttgag	120
94 atgcgcacac	tggtcaccc	tgcacccctc	aatatttcgg	cggaaaggccc	aacgatttgc	180
95 qtgcaccagt	ccgatgacca	gcttgcgtcty	atggatgagt	ggaaacgtcg	tacccatacc	240
96 ggcagcggyc	tggtggaaacg	cgtaaggcc	agcacccctgg	gogaccgcga	agcggagctg	300
97 ggcacgcgtt	aatttctgaa	gcagtggttgc	ccggcaggaa	aatccgttat	ctgtgggcaa	360
98 cagcatttgt	caggatctgc	gtttccctgtt	taa			393
100 <210>	SEQ ID NO:	6				
101 <211>	LENGTH:	675				
102 <212>	TYPE:	DNA				
103 <213>	ORGANISM:	Enterobacter cloacae				
105 <400>	SEQUENCE:	6				
106 cccctccgc	tgtccctggca	gtcgggtgg	aagacatccg	ccacccctttt	ccacaacatc	60
107 accctgggc	ca agctgtcgct	gctgtttctt	ggctgtgggg	tccgtatgc	cgccatcagg	120
108 cgttccctgc	tcatgtctca	ccctccctt	ctgagcgatg	ggctgtttaa	tttctgtgg	180
109 atgcagaccc	tgttctacat	tcccttttc	ctgatgggg	cgctggcatt	tattcatccc	240
110 cggcttaaag	cgtctgttac	cacccttcc	ccctgggtgt	cggtgggtgc	tgcgttggcc	300
111 ttgcgcgcot	atcttcctaa	tcagcgat	ggcagcgggg	acgcgtggat	gtatgaaaca	360
112 gagagcgtt	taacgtatcg	gtatggctg	tgatgttga	acgtgggtt	cgcccttggc	420
113 catcgcttc	tgaatttaa	atccagtc	gtcacctatt	tctttaatgc	ttagctgttt	480
114 atctacctgg	ttcaccatcc	gctgacgt	tttctgggg	cgtacattac	gccgcata	540
115 gcttcgaatg	cgtctggcgtt	cttcacccgc	ctggcttttg	tggttggcat	tgccatcgt	600
116 ttgtatgaaa	tccacccgtcg	gatcccgctt	ttgcgtttcc	tgttctcagg	caaacccat	660
117 gttaaaggcg	gataaa					675
119 <210>	SEQ ID NO:	7				
120 <211>	LENGTH:	647				
121 <212>	TYPE:	DNA				
122 <213>	ORGANISM:	Enterobacter cloacae				

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124 <220> FEATURE:  

125 <221> NAME/KEY: unsure  

126 <222> LOCATION: (41)  

128 <220> FEATURE:  

129 <221> NAME/KEY: unsure /  

130 <222> LOCATION: (54)  

132 <220> FEATURE:  

133 <221> NAME/KEY: unsure /  

134 <222> LOCATION: (60)  

136 <400> SEQUENCE: 7  

W--> 137 ggccgttcgt tccagtgaaa ttacccgtaa ccgacgtttt ntccgcggca gttnttctcn' 60
138 ttctccctgt ggatcattt cgtggaaaaaag qcgggttgtca gaggggtgttt atgagaccgc 120
139 aaatcgacgt tattatggc gataatcacya cgggtgcgtgt tgacgtgtatc gtcaacgcag 180
140 ccaatttcctc cctgtatgggt ggtggcgggg tgacgcgtgc cattcacccg qccgcaggcc 240
141 ctcaactcct tgaacatgc aaaaccgtgc gtcagcagca gggagagtgc cccgcggggc 300
142 atgtgttat tacgcttgcg ggcgatctcc cggccaaagc ggtgtatccat accgttggac 360
143 ccqtcgtgca cgggtggcgac cgccatgggg ctggagatctt qgagcaggcg tategttaact 420
144 gcatgcggtc tycggggat aacgggtata agaccatggc gttccccgc attagcaccg 480
145 ggggttccgg ctatccaaag gaagcggcag ctgcgtatgc ctgtataccat gtttatcaat 540
146 acctttccct caaaccatg ccggaaaaaaat tcattttgt ctgtttcgtat gagcacaccg 600
147 ccgacctgtt tcaagcggatt ttgacccgcgc gcaagcggc 647
149 <210> SEQ ID NO: 8
150 <211> LENGTH: 924
151 <212> TYPE: DNA
152 <213> ORGANISM: Enterobacter cloacae
154 <400> SEQUENCE: 8
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156 cgctcgctgg aycagggccgt cggccgcacccg ttccgggatt tctttggcg caataatggc 120
157 tggctgatcc tgcgtgtat tgcgttttat aagcttcggc acgttttcgc catgagtctg 180
158 accaccatcttccgtatccg ccggcgtcggtt tttgtatcggtt gggaggttcgg cgtgtgtac 240
159 aaaaccctgg ggctgtttgc cacgtatcgcc ggcgcgtgt acggccggcg attgtatgcg 300
160 cqgtctgtgc ttttcgtgc tctgtgtatc ttcggcattt ttcaggccgc ttcgaaatggc 360
161 ggttacttgc tgctgtatc caccgacaatg catatgtatca gcatggcgac ggcggatattc 420
162 tttgaaatc tgcgtgtatc ttttttttttttgcataatggc ggcgttgcgatggcgtatc 480
163 tgcaataatc ctttttcgc caccatgtt gcctgtatcc ctgccttcgc acggcgtcg 540
164 cgcgtgtatc taggttccgtt ccggggctgg tttgttgcgg cccacggctg gccgacattt 600
165 tatctcttctt cgggtggcgc ggcgtgtccg gggattttat tttgtgtgtt ctgtcgccag 660
166 acyctggat ataccacgg gacggaaacac ttcatggccg qacggaaata tcaagggtgcc 720
167 taccgggttg ccctgtgtatc gtcgtatggca ggttgttctt cgtgtgtatg gtgggtcg 780
168 gtactatgttcaatggac gaccacccgtt tgcgtttctt ttgaaaccca gtcgttgc 840
169 qcaggcggtgt ttctcgccat cgtgggtatc ctgaccgggtg ggtatgttgcgat 900
170 ctgcggaaaaa cgcagatgac atga 924
172 <210> SEQ ID NO: 9
173 <211> LENGTH: 1005
174 <212> TYPE: DNA
175 <213> ORGANISM: Enterobacter cloacae
177 <220> FEATURE:  

178 <221> NAME/KEY: unsure  

179 <222> LOCATION: (997)

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Input Set : D:\Pat9903.pto
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234 <222> LOCATION: (672)
236 <400> SEQUENCE: 11
237 cgtgagccga ccaacgggaa caccatgact ctgcctt ttattaacgc ctcccctgcc 60
238 ctgcggcgcga caggccatgc ggctggctg gactacggcc qcgcgcttc gctacgcgaa 120
239 atggccggc actacacccga gctgccaaaa tatctgtgg ctccggaaat ggeccgyactg 180
240 ctgcactttg ttcaggactg gggtcaagcac gctttttta atacgttatg gaataccggg 240
241 qcacgcctqa acgaaggcct tgccctgaga cgccgtgact ttccaccta cgaaqagcatt 300
242 ccgcattgtcg ttcttcgtc cgcacaaacag cgccgtgccc gggccggccg tccgcgttaag 360
243 gaaaaaagggtt ccaacccggg ggttgcgtta tcgacccgg cctatgtcga tgagatgcgc 420
244 cggtgttcg ccacgcacaa ggacgcgtt gaagatgtc cgattacagg cgaacgtcgc 480
245 geccaacccgg tggtaatgt ttccgaccgg acgggtgcgtg actggctgtt cggggcact 540
246 qatgccgcgg atcgtgacgg cgtcagactg agcatgcacg ttagccccca taccttccgg 600
247 cacagttttgc caatgcaccc ttatatggc cacgttcacc ctaaggactt ccaqqgtctg 660
W--> 248 ctggggccatg anaagttga gaggacttgc gtttatacga aaatatttgc gtcgacgtg 720
249 gctgcgcgtc acgacgtcg 660
250 <210> SEQ ID NO: 12
251 <211> LENGTH: 951
252 <212> TYPE: DNA
253 <213> ORGANISM: Enterobacter cloacae
254 <220> FEATURE:
255 <221> NAME/KEY: unsure
256 <222> LOCATION: (937)
257 <210> SEQ ID NO: 12
258 <211> LENGTH: 12
259 <212> TYPE: DNA
260 <213> ORGANISM: Enterobacter cloacae
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262 tctaattggcc ctatgaagtt aaatggaaaca tcttctgtat cttatggaaa attagaact 120
263 ctctttttcc cggatgttat aaatggaaa cattatgtgg ataaaggatgtg gtatctttt 180
264 gttctagcaa aggacccctt tggatccaa gaaatggatc caaagatggc tggccgtgtt 240
265 tccaaaacta aaacccgttca tcgagctccg ctgaacaaag actacatacc aaatccccca 300
266 atacttggaaac aagtggttaa actgttttac agtccggata tagatggaaat tgggtgtt 360
267 aaatggatgtt cccgttgcgaa acgactgaa atggtaatgtt acatggatcca catgtgaaat 420
268 tggccgttca caatggaa gatcaacacg aatattccgg tggatggatc tggaggtgag 480
269 cgcagtttta atgggtttaa tacagggtttt gtacacagcg atttggtaac gggatttctg 540
270 aatggtcacc tcatttttgc ggtatggatc gacaaatgc atcttgcatac ggcagcaaaa 600
271 ctccacatgc ccatttgaaacg taaggccctgg tcaactcgatc ctaatgggtt tggaggttata 660
272 actgtcaatgc gtcacacggc atttattttgtt actgtcaacaa caaacatgg tggaggcgct 720
273 cgcgggttcg tttcttcgtca acgtcaatgtt gcaatgggttta taaagggtt cttgtatgtt 780
274 gaaatggaga agcccgacaa agttgtttt accaatgtgc ttactaaacg atatagctct 840
275 ttgccttttc aggttcatgtt gaaatgggttta agatgtggc tggcgttaaa tggactctgg 900
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278 <211> LENGTH: 519
279 <212> TYPE: DNA
280 <213> ORGANISM: Enterobacter cloacae
281 <220> FEATURE:
282 <221> NAME/KEY: unsure
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285 gaaaacctga attacgcgtt tgaaaacttta gtggccgtt tcggcagcca cggcatcact 120
286 caacagcaat ccgcggact tggcagaacg gcaacgcac cggcaacca gaaagcgatc 180
287 gcaatctgg tatacggtgg tgagtggggaa aaagaacacc ttggcaatca ggtcgctgg 240
288 gatggcttgcgaaatcgccgg tggccgttgcgaaacatggc cggccgttgcgaaactatgc 300

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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Input Set : D:\Pat9903.pto
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L:56 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:2
L:56 M:340 W: (46) "n" or "Xaa" uscd: Feature required, for SEQ ID#:2
L:137 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:137 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:7
L:198 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:9
L:198 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
L:248 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:11
L:248 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:11
L:276 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:12
L:276 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:12
L:561 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:561 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:562 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:577 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:15
L:577 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:15
L:611 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:16
L:611 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:16
L:641 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:17
L:641 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:17
L:670 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:18
L:670 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:18
L:724 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:22
L:724 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:22
L:816 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:28
L:816 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:28
L:904 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:32
L:904 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:32
L:974 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:36
L:974 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:36
L:1188 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:49
L:1188 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:49
L:1233 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:52
L:1233 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:52
L:1327 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:57
L:1327 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:57
L:1369 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:60
L:1369 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:60
L:1423 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:62
L:1423 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:62
L:1458 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:64
L:1458 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:64
L:1577 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:72
L:1577 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:72
L:1581 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:72
M:340 Repeated in SeqNo=72
L:1610 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:74
L:1610 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:74

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L:1661 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:75
 L:1661 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:75
 L:1890 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:88
 L:1890 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:88
 L:2101 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:100
 L:2101 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:100
 L:2118 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:101
 L:2118 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:101
 L:2166 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:102
 L:2166 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:102
 L:2194 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:103
 L:2194 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:103
 L:2195 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:103
 M:340 Repeated in SeqNo=103
 L:2368 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:113
 L:2368 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:113
 L:2562 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:122
 L:2562 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:122
 L:2657 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:127
 L:2657 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:127
 L:2675 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:127
 M:340 Repeated in SeqNo=127
 L:2676 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:127
 L:2827 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:134
 L:2827 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:134
 L:2859 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:135
 L:2859 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:135
 L:2860 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:135
 M:340 Repeated in SeqNo=135
 L:3073 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:148
 L:3073 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:148
 L:3096 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:149
 L:3096 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:149
 L:3178 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:152
 L:3178 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:152
 L:3295 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:156
 L:3295 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:156
 L:3297 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:156
 M:340 Repeated in SeqNo=156
 L:3298 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:156
 L:3299 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:156
 L:3346 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:158
 L:3346 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:158
 L:3526 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:160
 L:3526 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:160
 L:3529 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:160
 M:340 Repeated in SeqNo=160
 L:3530 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:160
 L:3699 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:161

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/252,691C

DATE: 11/28/2000
TIME: 12:05:31

Input Set : D:\Pat9903.pto
Output Set: N:\CRF3\11282000\I252691C.raw

M:340 Repeated in SeqNo=161
L:4214 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:189
L:4231 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:190

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